

SEQUENCE LISTING

APPLICANT

TITLE OF INVENTION: Trehalose Synthase/Protein, Gene, Plasmids, Microorganisms, and A Process for Producing Trehalose

CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

22

FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Hak Hyun and Hwang, Ju Myung
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

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INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 4753
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: Trehalose Synthase Gene

HYPOTHETICAL:

ANTI-SENSE:

ORIGINAL SOURCE:

ORGANISM: Pseudomonas stutzeri
STRAIN: CJ38

SEQUENCE DESCRIPTION: SEQ ID NO: 1

GATCGCTGGC GTACTGCAGG TAGAGCAGGC GCATCGGCC CCAGGGCGCA TCGGCCGGCT	60
CCGCTGTGCC CTGCTGGTTC ATGAAGCGGA CGAAGCGGCC ATCGCGGAAC CGTGGACGCC	120
ATTCGGGGCT GTCCGGGTCG CGGCTGTCTCG TGAGCGTTCG CCACAGGTCG CTGCGAAACG	180
GCGGACCGCT CCAAAGCGCG CCGTGGATGG GATCGCCGAG CAGTTCGTGC AGCTCCCAGG	240
AACGTTGCGA ATGCAGCGCG CCGAGGCTCA GGCCATGCAG ATACAGGCGC GGTCGGCGTT	300
CGGCCGGCAG TTCGGTCCAG TAGCCATAGA TCTCGGCGAA TAGCGCGCGG GCCACGTTCG	360
GGCCGTAGTC GGCTCCACC AGCAGCGCCA GCGGGCTGTT CAGATAGGAG TACTGCAACG	420
CCACGTGGC GATATCGCCG TGGTGCAGGT ATTCCACTGC GTTCATCGCC GCCGGGTCGA	480
TCCAGCCGGT ACCGGTGGGC GTCACCAGCA CCAGCACC GA TCGCTCGAAG GCCTCGCTGC	540

3.

GCTGCAGCTC GCGCAAGGCC AGACGCGCCC GCTGGCGCGG GGTCTCTGCC GCGCGCAGAC 600
 CGACGTAGAC GCGAATCGGC TCGAGCGCGG AGCGGCCGCT CAAGACGCTG ATATCCGCCG 660
 CCGACGGGCC GGAGCCGATG AACTCGCGGC CGGTGCGGCC CAGCTCCTCC CAGCGCAGCA 720
 ACGAGGCCCG GCTGCCGCTT TTCAGCGCGG AGGCCGGTGG CGCGTCTCC GGTTCGATCA 780
 GGGGTCGTA CTGCGGAAG GATGCGTCCA GCATGCGCAG TGCCCGCGCC GCCAGCACAT 840
 CGCTGAGCAG CGACCAGAAC AGCGCCAGCG CCACCAGCAC GCCGATCACG TTGGCCAGGC 900
 GCGTGGCAG CACGCGGTCG GCGTGCCGCG AGACGAAGCG CGACACCAGC CGATACAGAC 960
 GCGCCAGCGT CAGCAGGATG AGAAAGGTG CCAGCGCGGT GAGAATGACT TCGAGCAGGT 1020
 GCGCACTGCT CACCGCGGC ATGCCATCA GCGCGGTAC CGCGTTCTGC CAGCCGGCGA 1080
 CCTGGCTGAG GAAATACCCG GCCAGCAGCA GGCAGCCGAC CGCGATCAGC AGATTGACCC 1140
 GCTCGCGCTG CCAGCCTGGG CGCTCCGCA GTTCCAGATA GCGCCACAGC CAGCGCCAGA 1200
 ACACGCCGAG GCCATAGCCC ACCGCCAGCG CCGCGCCGCG CAGCACGCC TGGTCAGCG 1260
 TCGAGCGCGG CAGCAGCGAT GCGTCAGCG CCGCGCAGAA GAACAGCGTG CCCAGCAGCA 1320
 GGCGAAACC GGACAGCGAG CGCCAGATAT AGAGGACGGG CAGGTGCAGC ATGAAGATCT 1380
 CCGCGTCCG GTGACGGCGT CGCGCCTCGG CATATCGAGG CGTGTCCGGT CGTCCGGTTC 1440
 CCGTGATGGT CCGCAGCAGG CCAATCCGAT GCAACGATGG CCGAGCGGCC GACTCAAACG 1500
 TCTACATTTC CCTAGTGCTG CCGGAACCGA TCGCCG 1536

ATG AGC ATC CCA GAC AAC ACC TAT ATC GAA TGG CTG GTC AGC CAG TCC 1584
 Met Ser Ile Pro Asp Asn Thr Tyr Ile Glu Trp Leu Val Ser Gln Ser

ATG CTG CAT GCG GCC CGC GAG CGG TCG CGT CAT TAC GCC GGC CAG GCG 1632
 Met Leu His Ala Ala Arg Glu Arg Ser Arg His Tyr Ala Gly Gln Ala

CGT CTC TGG CAG CGG CCT TAT GCC CAG GCC CGC CGC GAT GCC AGC 1680
 Arg Leu Trp Gln Arg Pro Try Ala Gln Ala Arg Pro Arg Asp Ala Ser

GCC ATC GCC TCG GTG TGG TTC ACC GCC TAT CCG GCG GCC ATC ATC ACG 1728
 Ala Ile Ala Ser Val Trp Phe Thr Ala Tyr Pro Ala Ala Ile Ile Thr

CCG GAA GGC GGC ACG GTA CTC GAG GCC CTC GGC GAC GAC CGC CTC TGG 1776
 Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly Asp Asp Arg Leu Trp

AGT GCG CTC TCC GAA CTC GGC GTG CAG GGC ATC CAC AAC GGG CCG ATG 1824
 Ser Ala Leu Ser Glu Leu Gly Val Gln Gly Ile His Asn Gly Pro Met

AAG CGT TCC GGT GGC CTG CGC GGA CGC GAG TTC ACC CCG ACC ATC GAC 1872
 Lys Arg Ser Gly Gly Leu Arg Gly Arg Glu Phe Thr Pro Thr Ile Asp

GGC AAC TTC GAC CGC ATC AGC TTC GAT ATC GAC CCG AGC CTG GGG ACC 1920
 Gly Asn Phe Asp Arg Ile Ser Phe Asp Ile Asp Pro Ser Leu Gly Thr

GAG GAG CAG ATG CTG CAG CTC AGC CGG GTG GCC GCG GCG CAC AAC GCC 1968
 Glu Glu Gln Met Leu Gln Leu Ser Arg Val Ala Ala Ala His Asn Ala

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4.

ATC GTC ATC GAC GAC ATC GTG CCG GCA CAC ACC GGC AAG GGT GCC GAC Ile Val Ile Asp Asp Ile Val Pro Ala His Thr Gly Lys Gly Ala Asp	2016
TTC CGC CTC GCG GAA ATG GCC TAT GGC GAC TAC CCC GGG CTG TAC CAC Phe Arg Leu Ala Glu Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His	2064
ATG GTG GAA ATC CGC GAG GAG GAC TGG GAG CTG CTG CCC GAG GTG CCG Met Val Glu Ile Arg Glu Glu Asp Trp Glu Leu Leu Pro Glu Val Pro	2112
GCC GGG CGT GAT TCG GTC AAC CTG CTG CCG CCG GTG GTC GAC CGG CTC Ala Gly Arg Asp Ser Val Asn Leu Leu Pro Pro Val Val Asp Arg Leu	2160
AAG GAA AAG CAC TAC ATC GTC GGC CAG CTG CAG CGG GTG ATC TTC TTC Lys Glu Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe	2208
GAG CCG GGC ATC AAG GAC ACC GAC TGG AGC GTC ACC GGC GAG GTC ACC Glu Pro Gly Ile Lys Asp Thr Asp Trp Ser Val Thr Gly Glu Val Thr	2256
GGG GTC GAC GGC AAG GTG CGT CGC TGG GTC TAT CTG CAC TAC TTC AAG Gly Val Asp Gly Lys Val Arg Arg Trp Val Tyr Leu His Tyr Phe Lys	2304
GAG GGC CAG CCG TCG CTG AAC TGG CTC GAC CCG ACC TTC GCC GCG CAG Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala Ala Gln	2352
CAG CTG ATC ATC GGC GAT GCG CTG CAC GCC ATC GAC GTC ACC GGC GCC Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val Thr Gly Ala	2400
CGG GTG CTG CGC CTG GAC GCC AAC GGC TTC CTC GGC GTG GAA CGG CGC Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly Val Glu Arg Arg	2448
GCC GAG GGC ACG GCC TGG TCG GAG GGC CAC CCG CTG TCC GTC ACC GGC Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro Leu Ser Val Thr Gly	2496
AAC CAG CTG CTC GCC GGG GCG ATC CGC AAG GCC GGC GGC TTC AGC TTC Asn Gln Leu Leu Ala Gly Ala Ile Arg Lys Ala Gly Gly Phe Ser Phe	2544
CAG GAG CTG AAC CTG ACC ATC GAT GAC ATC GCC GCC ATG TCC CAC GGC Gln Glu Leu Asn Leu Thr Ile Asp Asp Ile Ala Ala Met Ser His Gly	2592
GGG GCC GAT CTG TCC TAC GAC TTC ATC ACC CGC CCG GCC TAT CAC CAT Gly Ala Asp Leu Ser Tyr Asp Phe Ile Thr Arg Pro Ala Tyr His His	2640
GCG TTG CTC ACC GGC GAT ACC GAA TTC CTG CGC ATG ATG CTG CGC GAA Ala Leu Leu Thr Gly Asp Thr Glu Phe Leu Arg Met Met Leu Arg Glu	2688

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5:

GTG CAC GCC TTC GGC ATC GAC CCG GCG TCA CTG ATC CAT GCG CTG CAG Val His Ala Phe Gly Ile Asp Pro Ala Ser Leu Ile His Ala Leu Gln	2736
AAC CAT GAC GAG TTG ACC CTG GAG CTG GTG CAC TTC TGG ACG CTG CAC Asn His Asp Glu Leu Thr Leu Glu Leu Val His Phe Trp Thr Leu His	2784
GCC TAC GAC CAT TAC CAC TAC AAG GGC CAG ACC CTG CCC GGC GGC CAC Ala Tyr Asp His Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His	2832
CTG CGC GAA CAT ATC CGC GAG GAA ATG TAC GAG CGG CTG ACC GGC GAA Leu Arg Glu His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu	2880
CAC GCG CCG TAC AAC CTC AAG TTC GTC ACC AAC GGG GTG TCC TGC ACC His Ala Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys Thr	2928
ACC GCC AGC GTG ATC GCC GCG GCG CTT AAC ATC CGT GAT CTG GAC GCC Thr Ala Ser Val Ile Ala Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala	2976
ATC GGC CCG GCC GAG GTG GAG CAG ATC CAG CGT CTG CAT ATC CTG CTG Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His Ile Leu Leu	3024
GTG ATG TTC AAT GCC ATG CAG CCC GGC GTG TTC GCC CTC TCC GGC TGG Val Met Phe Asn Ala Met Gln Pro Gly Val Phe Ala Leu Ser Gly Trp	3072
GAT CTG GTC GGC GCC CTG CCG CTG GCG CCC GAG CAG GTC GAG CAC CTG Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu Gln Val Glu His Leu	3120
ATG GGC GAT GGC GAT ACC CGC TGG ATC AAT CGC GGC GGC TAT GAC CTC Met Gly Asp Gly Asp Thr Arg Trp Ile Asn Arg Gly Gly Tyr Asp Leu	3168
GCC GAT CTG GCG CCG GAG GCG TCG GTC TCC GCC GAA GGC CTG CCC AAG Ala Asp Leu Ala Pro Glu Ala Ser Val Ser Ala Glu Gly Leu Pro Lys	3216
GCC CGC TCG CTG TAC GGC AGC CTG GCC GAG CAG CTG CAG CGG CCA GGC Ala Arg Ser Leu Tyr Gly Ser Leu Ala Glu Gln Leu Gln Arg Pro Gly	3264
TCC TTC GCC TGC CAG CTC AAG CGC ATC CTC AGC GTG CGC CAG GCC TAC Ser Phe Ala Cys Gln Leu Lys Arg Ile Leu Ser Val Arg Gln Ala Tyr	3312
GAC ATC GCT GCC AGC AAG CAG ATC CTG ATT CCG GAT GTG CAG GCG CCG Asp Ile Ala Ala Ser Lys Gln Ile Leu Ile Pro Asp Val Gln Ala Pro	3360
GGA CTC CTG GTG ATG GTC CAC GAG CTG CCT GCC GGC AAG GGC GTG CAG Gly Leu Leu Val Met Val His Glu Leu Pro Ala Gly Lys Gly Val Gln	3408

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6/

CTC ACG GCA CTG AAC TTC AGC GCC GAG CCG GTC AGC GAG ACC ATC TGC 3456
Leu Thr Ala Leu Asn Phe Ser Ala Glu Pro Val Ser Glu Thr Ile Cys

CTG CCC GGC GTG GCG CCC GGC CCG GTG GTG GAC ATC ATT CAC GAG AGT 3504
Leu Pro Gly Val Ala Pro Gly Pro Val Val Asp Ile Ile His Glu Ser

GTG GAG GGC GAC CTC ACC GAC AAC TGC GAG CTG CAG ATC AAC CTC GAC 3552
Val Glu Gly Asp Leu Thr Asp Asn Cys Glu Leu Gln Ile Asn Leu Asp

CCG TAC GAG GGG CTT GCC CTG CGT GTG GTG AGC GCC GCG CCG CCG GTG 3600
Pro Tyr Glu Gly Leu Ala Leu Arg Val Val Ser Ala Ala Pro Pro Val

ATC TGA GCGC 3610
Ile

CCTCTTGGCG CGCCCCGGGT CCGCCGCTAT AGTGCGCAGC GCCTGGGGCG CGCATTGCCC 3670

TCGCCGTGCA GACCAGCCCG TGTCGTTTTC TTCGCTTTTC CGCCTTGCGC TGCTGCCGCT 3730

GGCGCTGCTT GCGCACCCG TCTGGGCGCA GACCGCTGC CCGCCCGGCC AGCAGCCGAT 3790

CTGCCGTAGC GGCAGCTGCC TCTGCGTGCC GCGCGCCGCC AGCGATCCAC AGGCGGTCTA 3850

CGACCGCGTG CAGCGTATGG CTACGCTGGC CCTGCAGAAC TGGATCCAGC AGTCGCGCGA 3910

CCGCCTGATG GCGGGCGGCG TCGAGCCGAT ACCGCTGCAC ATCCGCTCGC AGCTCGAGCC 3970

GTATTTGAT CTTGCCGTGC TGGAGAGTGC GCGGTACCGC GTCGGCGACG AGGTGGTGCT 4030

GACTGCCGGC AACACCCTGC TGGCAACCC GGACGTCAAT GCGGTGACCC TGATCGACGT 4090

CATCGTCTTC CGCCACGAGG AGGATGCCCG GGACAACGTC GCGCTCTGGG CCCATGAGCT 4150

CAAGCACGTC GAGCAATATC TGGACTGGGG CGTCGCCGAG TTCGCCCGGC GCTATACGCA 4210

GGATTTCCGT GCGGTGGAGC GCCCGGCCCTA TGCCTGGAG CGTGAGGTGG AAGAGGCCCT 4270

GCGCGAGACG CAGACGCGGC GCTGAGCGAG CTGATCGGTG CTGCTGCCCG CACTGGGCTG 4330

AAGCCACCA ATGACGCCGG CGAAAACGAA AAACCCCGCC GAGGCGGGGT TTCTGACGCG 4390

GGTTGTGCGG TCAGCTCAGA ACGCCGGGAC CACGGCGCCC TTGTACTTTT CCTCGATGAA 4450

CTGGCGTACT TGCTCGCTGT GCAGCGCGGC AGCCAGTTTC TGCATGGCAT CGCTGTCCCT 4510

GTTGTCCGA CGGGCGACCA GAATGTTTAC GTATGGCGAG TCGCTGCCCT CGATCACCAG 4570

GGCGTCCTGG GTCGGGTTCA GCTTGGCTTC CAGCGCGTAG TTGGTGTTGA TCAGCGCCAG 4630

GTCGACCTGG GTCAGCACGC GCGGCAGAGT CGCGGCTTCC AGTTGCGGGA TCTTGATCTT 4690

CTTCGGGTTT TCGGCGATGT CTTGGGCGTG GCGGTGATGC CGGCGCCGTC CTTAGACCG 4750

ATC 4753

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